

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

(i) APPLICANTS: June, Carl H. and Thompson, Craig B.

(ii) TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL
BY AUGMENTING BCL-XL PROTEIN LEVELS

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(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

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- (A) ADDRESSEE: LAHIVE & COCKFIELD
- (B) STREET: 60 State Street, Suite 510
- (C) CITY: Boston
- (D) STATE: Massachusetts
- (E) COUNTRY: USA
- (F) ZIP: 02109-1875

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(v) COMPUTER READABLE FORM:

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- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

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- (A) APPLICATION NUMBER: US
- (B) FILING DATE:

(vii) PRIOR APPLICATION DATA:

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- (A) APPLICATION NUMBER: US
- (B) FILING DATE: 04-MAY-1995

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: DeConti, Giulio A. (GAD)
- (B) REGISTRATION NUMBER: 31,503
- (C) REFERENCE/DOCKET NUMBER: RPI-034CP

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(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (617)227-7400
- (B) TELEFAX: (617)227-5941

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 926 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 135..836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5	GAATCTCTTT CTCTCCCTTC AGAATCTTAT CTTGGCTTTG GATCTTAGAA GAGAATCACT	60
	AACCAGAGAC GAGACTCAGT GAGTGAGCAG GTGTTTTTGA CAATGGACTG GTTGAGCCCA	120
10	TCCCTATTAT AAAA ATG TCT CAG AGC AAC CGG GAG CTG GTG GTT GAC TTT	170
	Met Ser Gln Ser Asn Arg Glu Leu Val Val Asp Phe	
	1 5 10	
15	CTC TCC TAC AAG CTT TCC CAG AAA GGA TAC AGC TGG AGT CAG TTT AGT	218
	Leu Ser Tyr Lys Leu Ser Gln Lys Gly Tyr Ser Trp Ser Gln Phe Ser	
	15 20 25	
20	GAT GTG GAA GAG AAC AGG ACT GAG GCC CCA GAA GGG ACT GAA TCG GAG	266
	Asp Val Glu Glu Asn Arg Thr Glu Ala Pro Glu Gly Thr Glu Ser Glu	
	30 35 40	
25	ATG GAG ACC CCC AGT GCC ATC AAT GGC AAC CCA TCC TGG CAC CTG GCA	314
	Met Glu Thr Pro Ser Ala Ile Asn Gly Asn Pro Ser Trp His Leu Ala	
	45 50 55 60	
30	GAC AGC CCC GCG GTG AAT GGA GCC ACT GGC CAC AGC AGC AGT TTG GAT	362
	Asp Ser Pro Ala Val Asn Gly Ala Thr Gly His Ser Ser Ser Leu Asp	
	65 70 75	
35	GCC CGG GAG GTG ATC CCC ATG GCA GCA GTA AAG CAA GCG CTG AGG GAG	410
	Ala Arg Glu Val Ile Pro Met Ala Ala Val Lys Gln Ala Leu Arg Glu	
	80 85 90	
40	GCA GGC GAC GAG TTT GAA CTG CGG TAC CGG CGG GCA TTC AGT GAC CTG	458
	Ala Gly Asp Glu Phe Glu Leu Arg Tyr Arg Arg Ala Phe Ser Asp Leu	
	95 100 105	
45	ACA TCC CAG CTC CAC ATC ACC CCA GGG ACA GCA TAT CAG AGC TTT GAA	506
	Thr Ser Gln Leu His Ile Thr Pro Gly Thr Ala Tyr Gln Ser Phe Glu	
	110 115 120	
50	CAG GTA GTG AAT GAA CTC TTC CGG GAT GGG GTA AAC TGG GGT CGC ATT	554
	Gln Val Val Asn Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile	
	125 130 135 140	
55	GTG GCC TTT TTC TCC TTC GGC GGG GCA CTG TGC GTG GAA AGC GTA GAC	602
	Val Ala Phe Phe Ser Phe Gly Gly Ala Leu Cys Val Glu Ser Val Asp	
	145 150 155	
60	AAG GAG ATG CAG GTA TTG GTG AGT CGG ATC GCA GCT TGG ATG GCC ACT	650
	Lys Glu Met Gln Val Leu Val Ser Arg Ile Ala Ala Trp Met Ala Thr	
	160 165 170	
65	TAC CTG AAT GAC CAC CTA GAG CCT TGG ATC CAG GAG AAC GGC GGC TGG	698
	Tyr Leu Asn Asp His Leu Glu Pro Trp Ile Gln Glu Asn Gly Gly Trp	
	175 180 185	
70	GAT ACT TTT GTG GAA CTC TAT GGG AAC AAT GCA GCA GCC GAG AGC CGA	746
	Asp Thr Phe Val Glu Leu Tyr Gly Asn Asn Ala Ala Ala Glu Ser Arg	
	190 195 200	

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AAG GGC CAG GAA CGC TTC AAC CGC TGG TTC CTG ACG GGC ATG ACT GTG 794
 Lys Gly Gln Glu Arg Phe Asn Arg Trp Phe Leu Thr Gly Met Thr Val
 205 210 215 220
 5
 GCC GGC GTG GTT CTG CTG GGC TCA CTC TTC AGT CGG AAA TGACCAGACA 843
 Ala Gly Val Val Leu Leu Gly Ser Leu Phe Ser Arg Lys
 225 230
 10 CTGACCATCC ACTCTACCCT CCCACCCCCT TCTCTGCTCC ACCACATCCT CCGTCCAGCC 903
 GCCATTGCCA CCAGGAGAAC CCG 926
 15 (2) INFORMATION FOR SEQ ID NO:2:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 amino acids
 (B) TYPE: amino acid
 20 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
 25 Met Ser Gln Ser Asn Arg Glu Leu Val Val Asp Phe Leu Ser Tyr Lys
 1 5 10 15
 30 Leu Ser Gln Lys Gly Tyr Ser Trp Ser Gln Phe Ser Asp Val Glu Glu
 20 25 30
 Asn Arg Thr Glu Ala Pro Glu Gly Thr Glu Ser Glu Met Glu Thr Pro
 35 35 40 45
 35 Ser Ala Ile Asn Gly Asn Pro Ser Trp His Leu Ala Asp Ser Pro Ala
 50 55 60
 Val Asn Gly Ala Thr Gly His Ser Ser Ser Leu Asp Ala Arg Glu Val
 40 65 70 75 80
 Ile Pro Met Ala Ala Val Lys Gln Ala Leu Arg Glu Ala Gly Asp Glu
 85 90 95
 45 Phe Glu Leu Arg Tyr Arg Arg Ala Phe Ser Asp Leu Thr Ser Gln Leu
 100 105 110
 His Ile Thr Pro Gly Thr Ala Tyr Gln Ser Phe Glu Gln Val Val Asn
 115 120 125
 50 Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe
 130 135 140
 Ser Phe Gly Gly Ala Leu Cys Val Glu Ser Val Asp Lys Glu Met Gln
 145 150 155 160
 55 Val Leu Val Ser Arg Ile Ala Ala Trp Met Ala Thr Tyr Leu Asn Asp
 165 170 175
 His Leu Glu Pro Trp Ile Gln Glu Asn Gly Gly Trp Asp Thr Phe Val

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Leu Leu Gly Ser Leu Phe Ser Arg Lys
225 230

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